region,

a second nucleotide sequence encoding an antibody light chain variable region,

a linker sequence encoding a linker peptide that links the antibody heavy chain variable region and the an antibody light chain variable region, and

~~a 5'- and 3'- flanking sequence~~ 5'- and 3'- flanking sequences at the ends of the insert sequence which are sufficiently homologous to the 5'- and 3'-terminus sequences of the linearized yeast expression vector, respectively, to enable homologous recombination to occur; and

having homologous recombination occur between the linearized yeast expression vector and the library of insert sequences to form a library of yeast expression vectors comprising the insert sequences in the transformed yeast cells;

wherein

the antibody heavy chain variable region, the antibody light chain variable region, and the linker polypeptide are expressed as a single fusion protein in the transformed yeast cells by the library of yeast expression vectors;

the first and second nucleotide sequences of the insert sequences each independently varies within the library of yeast expression vectors; and

the diversity of the insert sequences comprised in the library of yeast expression vectors is at least $1x10^7$.

2. (Amended) The method of claim 1, wherein the 5'- or 3'- flanking sequence of the insert nucleotide sequences is between 30-120 bp in length.

3. (Amended) The method of claim 1, wherein the 5'- or 3'- flanking sequence of the insert nucleotide sequences is between 40-90 bp in length.

4. (Amended) The method of claim 1, wherein the 5'- or 3'- flanking sequence of the insert nucleotide sequences sequences is between 60-80 bp in length.

5. (Amended) The method of claim 1, wherein the linker sequence of the insert nucleotide sequences is between 30-120 bp in length.

6. (Amended) The method of claim 1, wherein the linker sequence of the insert nucleotide sequences is between 45-102 bp in length.

7. (Amended) The method of claim 1, wherein the linker sequence of the insert nucleotide sequences is between 45-63 bp in length.

8. (Amended) The method of claim 1, wherein the linker sequence of the insert nucleotide sequences comprises a nucleotide sequence encoding an amino acid sequence of Gly-Gly-Gly-Gly-Ser [SEQ ID NO: 76] in 3 or 4 tandem repeats.

10. (Amended) The method of claim 1, wherein the diversity of the antibody heavy chain variable region or the antibody light chain variable region of the insert sequences comprised in the library of yeast expression vectors is at least 10^3.

11. (Amended) The method of claim 1, wherein the diversity of the antibody heavy chain variable region or the antibody light chain variable region of the insert sequences comprised in the library of yeast expression vectors is at least 10^4.

12. (Amended) The method of claim 1, wherein the diversity of the antibody heavy chain variable region or the antibody light chain variable region of the insert sequences comprised in the library of yeast expression vectors is at least 10^5.

13. (Amended) The method of claim 1, wherein the diversity of the insert sequences comprised in the library of yeast expression vectors is at least $1x10^8$.

14. (Amended) The library of claim 1, wherein the diversity of the insert sequences comprised in the library of yeast expression vectors is at least $1x10^{10}$.

15. (Amended) The method of claim 1, wherein the diversity of the insert sequences comprised in the library of yeast expression vectors is at least $1x10^{12}$.

24. (Amended) The method of claim 23, wherein the affinity tag is selected from the group consisting of a polyhistidine tag, polyarginine tag, glutathione-S-transferase, maltose binding protein, staphylococcal protein A tag, and an EE-epitope tag.

Please add the following new claims --

44. (New) The method of claim 1, wherein each insert nucleotide sequence in the library of insert nucleotide sequences is generated by an overlapping PCR which assembles

a first PCR fragment comprising in a 5' to 3' order the 5'- flanking sequence, the first nucleotide sequence, and the linker sequence; and

a second PCR fragment comprising in a 3' to 5' order the 3'- flanking sequence, the second nucleotide sequence, and the linker sequence

into a single fragment through the overlapping linker sequence of both the first and the second PCR fragments.

45. (New) The method of claim 1, wherein the first nucleotide sequence and the second nucleotide sequence respectively encode a heavy chain variable region and a light chain variable region of immunoglobulin genes of a human, non-human primates, or rodent.

46. (New) The method of claim 1, wherein the first nucleotide sequence and the second nucleotide sequence respectively encode a heavy chain variable region and a light chain variable region of a human immunoglobulin gene.

47. (New) The method of claim 1, the linearized yeast expression vector further comprising: a transcription sequence encoding an activation domain or a DNA binding domain of a transcription activator.

48. (New) The method of claim 47, wherein the transcription sequence is capable of being expressed as a fusion protein with the single fusion protein comprising the antibody heavy chain variable region, the antibody light chain variable region, and the linker polypeptide.

49. (New) The method of claim 47, wherein the transcription activator is a transcription activator having separable DNA-binding and transcription activation domains.

50. (New) The library of claim 49, wherein the transcription activator is selected from the group consisting of GAL4, GCN4, and ADR1 transcription activator. --.